MAR 1 1 200 Replacement Sheet Eg ttg ctg atc aac ttt ttc atc gct gtt ctg gga gtg ata tca ctg 48 Met Leu Leu Ile Asn Phe Phe Ile Ala Val Leu Gly Val Ile Ser Leu 10 15 tct cct att gtg gtt gct cgt tat att ctt cga cga gat tgc act aca 96 Ser Pro Ile Val Val Ala Arg Tyr Ile Leu Arg Arg†Asp Cys Thr Thr 20 25 gtt acg gtc ttg tcc tcc cct gag tct gtg acg agt tcg aac cat gtt Val Thr Val Leu Ser Ser Pro Glu Ser Val Thr Ser Ser Asn His Val 45 cag cta gcc agt cat gag atg tgc gac agt acc ttg tca gcg tcc ctt Gln Leu Ala Ser His Glu Met Cys Asp Ser Thr Leu Ser Ala Ser Leu 50 60 55 tat atc tac aat gat gat tat gat aag att gtg aca ctt tat tat ctt Tyr Ile Tyr Asn Asp Asp Tyr Asp Lys Ile Val Thr Leu Tyr Tyr Leu 80 70 75 65 aca tcg tcg ggc aca act ggg tcc gta aca gcg tct tat tct tct agt Thr Ser Ser Gly Thr Thr Gly Ser Val Thr Ala Ser Tyr Ser Ser Ser 85 90 95 ttg agt aac aac tgg gaa ttg tgg tct ctc tcg gct ccg gct gca gat Leu Ser Asn Asn Trp Glu Leu Trp Ser Leu Ser Ala Pro Ala Ala Asp 100 110 105 gct gtc gag atc act gga gct agt tat gta gac agc gat gca tct gcg Ala Val Glu Ile Thr Gly Ala Ser Tyr Val Asp Ser Asp Ala Ser Ala 115 120 125 aca tac gcc acg tct ttt gat ata cct ctt act acc acg aca acg tcg Thr Tyr Ala Thr Ser Phe Asp Ile Pro Leu Thr Thr Thr Thr Ser 140 130 135 tcg tct tct gct agt gcg act tca aca tct agt cta acc aca aca tct Ser Ser Ser Ala Ser Ala Thr Ser Thr Ser Ser Leu Thr Thr Ser 155 160 145 150 agt gtt tcc att tcg gtg tcc gtc cct aca gga aca gct gca aat tgg 528 Ser Val Ser Ile Ser Val Ser Val Pro Thr Gly Thr Ala Ala Asn Trp 165 170 175 cga ggt agg gct atc tat cag atc gtg act gat aga ttt gca cgc act Arg Gly Arg Ala Ile Tyr Gln Ile Val Thr Asp Arg Phe Ala Arg Thr 185 180 190

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FIG. 1a

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gac ggc tcc Asp Gly Ser 195							_				624
gga ggg tct Gly Gly Ser 210	-					_	_				672
atg ggc ttt Met Gly Phe 225	Thr Ala										720
gat gac acc Asp Asp Thr											768
atc ttc gcc Ile Phe Ala	_	Thr Asn	Phe	Gly	Thr	Ala	Asp	Asp	Leu		816
ttg gct acg Leu Ala Thr 275											864
gtt gtc aat Val Val Asn 290											912
tct gaa tat Ser Glu Tyr 305	-	_									960
tgg att aca Trp Ile Thr											1008
ggc gac gat Gly Asp Asp											1056
gtg aaa agt Val Lys Ser 355											1104
tct att gac Ser Ile Asp 370			Asp								1152

FIG. 1b

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ttt t Phe 7 385		_					_	_					_		-	1200
gta t Val <u>I</u>		•		_					_			_	_			1248
gac (_	_				_				_	_				1296
gag a Glu S	_	_	_		_	_		_		_	_	_		_	-	1344
ctc a	Lys	Ser	Glu	Cys	Thr	Asp	Thr	Thr	Leu	Leu	Gly		Phe	Leu	Glu	1392
aat o Asn 0 465				_	_			-				_				1440
att a Ile I					_			_			_	• •				1488
att t				_									_			1536
aat d Asn A	_						Thr	Gly		Ser		_	_	_		1584
tac a					_	_		_		_		_	_			1632
aaa q Lys <i>A</i> 545	-	•						_			_			_	_	1680
tcc a	_			-	_				Phe 570							1728

FIG. 1c

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_	_	_	tca Ser 580				_	 _	_		_	_	1776
	_		acg Thr									_	1824
	_		gct Ala			_	_			-			1872
_		_	ggc Gly			_		_	_	_	_	_	1920
			atc Ile	_	_	taga	ag						1946